

Sequence listing

<110> SHANGHAI CANCER INSTITUTE

<120> A HUMAN TUMOR-ASSOCIATED GENE CT120 ON CHROMOSOME 17P 13.3 REGION AND PROTEIN  
 ENCODED BY IT

<130> 024832pc

<150> CN 02150730.9

<151> 2002-11-27

<160> 13

<170> PatentIn version 3.1

<210> 1

<211> 2145

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(861)

<223>

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gccagcggagg	cggccggacc	cgcagcccg	atg	ctg	114
			Met	Leu	
			Leu	Thr	
			Leu	Ala	
			Gly	Gly	
			1	5	
gcg	ctc	ttc	ccg	ggg	162
Ala	Leu	Phe	Phe	Pro	
				Gly	
				Leu	
				Phe	
				Ala	
				Cys	
				Thr	
				Trp	
				Ala	
				Leu	
				Arg	
10	15	20			
cac	tcc	cag	ccc	gga	210
His	Ser	Gln	Pro	Gly	
				Trp	
				Ser	
				Arg	
				Thr	
25	30	35	40		
agg	ctg	gtt	tcc	tcg	258
Arg	Leu	Val	Ser	Val	
				His	
				Ala	
				Val	
				Leu	
				Ala	
				Thr	
				Gly	
				Ser	
				Ile	
45	50	55			
gtc	atc	att	cgc	tcc	306
Val	Ile	Ile	Arg	tgc	
			Ser	gac	
				gtg	
				acc	
				gcc	
				agg	
				cac	
				tgg	
60	65	70			
gcc	cg	gaa	tat	gtg	354
Ala	Arg	Glu	Tyr	ttt	
			Val	ctg	
				att	
				cca	
				tac	
				atg	
				atc	
75	80	85			
tac	gcc	atg	tac	ctc	402
Tyr	Ala	Met	Tyr	tgt	
			Leu	gaa	
				ttg	
				tgc	
				cga	
				acc	
				aga	
				gac	
				cag	
				aac	
				cgt	
90	95	100			
gcg	ccc	tcc	ctc	act	450
Ala	Pro	Ser	Leu	Thr	
				Leu	
				Arg	
				Asn	
				Arg	
105	110	115	120		
atc	aca	cat	cat	gcg	498
Ile	Thr	His	His	gtc	
				att	
				ctc	
				ctt	
				gtc	
				ctt	
				gtg	
				cca	
				gtc	
				gca	
				cag	
125	130	135			
agg	ctc	cgg	gga	gac	546
Arg	Leu	Arg	Gly	ctt	
			Asp	ttc	
			Leu	gtc	
			Gly	atc	
			Asp	ttc	
			Phe	gtc	
			Val	gtc	
			Gly	ttt	
			Cys	gtt	
			Ile	gtt	
			Phe	ctg	
140	145	150			
gca	gaa	ctg	agc	act	594
Ala	Glu	Leu	Ser	Thr	
				Pro	
				Phe	
				Val	
				Gly	
				Arg	
				Val	
				Leu	
				Ile	
				Gln	

155	160	165	
cta aag cag cag cac acc ctt ctg tac aag gtg aat gga atc ctc acg			642
Leu Lys Gln Gln His Thr Leu Leu Tyr Lys Val Asn Gly Ile Leu Thr			
170	175	180	
ctg gcc acc ttc ctt tcc tgc cgg atc ctt ctc ttc ccc ttc atg tac			690
Leu Ala Thr Phe Leu Ser Cys Arg Ile Leu Leu Phe Pro Phe Met Tyr			
185	190	195	200
tgg tcc tat ggc cgc cag cag gga cta agc ctg ctc caa gta ccc ttc			738
Trp Ser Tyr Gly Arg Gln Gln Gly Leu Ser Leu Leu Gln Val Pro Phe			
205	210	215	
agc atc cca ttc tac tgc aac gtg gcc aat gcc ttc ctc gta gct cct			786
Ser Ile Pro Phe Tyr Cys Asn Val Ala Asn Ala Phe Leu Val Ala Pro			
220	225	230	
cag atc tac tgg ttc tgt ctg ctg agg aag gca gtc cgg ctc ttt			834
Gln Ile Tyr Trp Phe Cys Leu Leu Cys Arg Lys Ala Val Arg Leu Phe			
235	240	245	
gac act ccc caa gcc aaa aag gat ggc taaatgctcc tgggagtcag			881
Asp Thr Pro Gln Ala Lys Lys Asp Gly			
250	255		
gcgcagcctc acaccagctg cctccctccac tcagcattcc atggaccaaa ttgtccccgt			941
ggtagcctca gactttgggt attgataagc cgatggattt gagttttct aaagaatatt			1001
catattacct ccttttcta acttgcctta ttgcaaaacg cactttgtt gtaacaacta			1061
ttgggtccctg tcagacctcc acggacagca aagtggttt aatgcaagcc caaggatcct			1121
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agggtggtaa gtgtctgcac atctgcctgt ccctgtatca gcccgtaccc accttccaaa			1241
ccactcagga cagtaccctt ggcactgggc cccgagaagc aaggatgac ttggttcttg			1301
gaagtaatgt cgttctgttga cattggctgg gacaaatcat tggggtagg tagttattga			1361
tcgtttacta gataaccat tgggttcttg cctcatcctc tcatccatgg gtcagagttt			1421
aattctttagt tctatagact tccaaatcaga agtctcaactg gtggggctgg ggggtggggc			1481
aggcaggagg catggatggg aacctgagta ggttggtagg ccaagagatc agcacaaccc			1541
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cagaggctgt tcttttccac acacccttc atgcccggct ttcccccataat ccacatgcag			1661
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aaccatgaaa tggatcatct agactcgaga gtactcgagt gctttgcctc cccgatatgcc			1841
agagcttgg tgcggaaagcc cattcctgtg tggccgtt gccatttagc cacagaagcc			1901
tgcggagctt ggcggcagctt agcctggcca gtggctgtcc cgtggaccga caccctgcgcc			1961
cccttctgcactt agcaggattt tctggtgcca acactcattt atcattcccg atcaactagg			2021
atgaattttaa gactgtgttca ccatgtgttca tcaagtggta gttaaaaag tggatttta			2081
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aaaa			2145

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 <212> PRT  
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 Thr Asp Cys Val Met Ile Ser Thr Arg Leu Val Ser Ser Val His Ala  
 35 40 45  
 Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp  
 50 55 60  
 Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu  
 65 70 75 80  
 Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp  
 85 90 95  
 Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn  
 100 105 110  
 Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu

115	120	125
Leu Val Leu Val Pro Val Ala Gln Arg Leu Arg Gly Asp Leu Gly Asp		
130	135	140
Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val		
145	150	155
Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu		
165	170	175
Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg		
180	185	190
Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly		
195	200	205
Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val		
210	215	220
Ala Asn Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu		
225	230	235
Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys Asp		
245	250	255
Gly		

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25

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23

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22

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<221> MISC\_FEATURE  
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<223> oligopeptide corresponding to C-terminus of CT120 protein

<400> 11

Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys  
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